OIPE

#14

RAW SEQUENCE LISTING DATE: 07/05/2001
PATENT APPLICATION: **US/09/670,756A** TIME: 10:39:36

Input Set : **A:\seqlistcorrected.txt**
Output Set: **N:\CRF3\07052001\I670756A.raw**

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  3 <110> APPLICANT: Rhodes, Kenneth
  4       Betty, Maria
  5       Ling, Huai-Ping
  6       An, Wenqian
  8 <120> TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
 10 <130> FILE REFERENCE: MNI-070CP4
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/670,756A
 13 <141> CURRENT FILING DATE: 2000-09-27
 15 <150> PRIOR APPLICATION NUMBER: USSN 60/110,277
 16 <151> PRIOR FILING DATE: 1998-11-30
 18 <150> PRIOR APPLICATION NUMBER: USSN 60/110,033
 19 <151> PRIOR FILING DATE: 1998-11-25
 21 <150> PRIOR APPLICATION NUMBER: USSN 60/109,333
 22 <151> PRIOR FILING DATE: 1998-11-20
 24 <150> PRIOR APPLICATION NUMBER: USSN 09/298,731
 25 <151> PRIOR FILING DATE: 1999-04-23
 27 <150> PRIOR APPLICATION NUMBER: USSN 09/350,614
 28 <151> PRIOR FILING DATE: 1999-07-09
 30 <150> PRIOR APPLICATION NUMBER: USSN 09/350,874
 31 <151> PRIOR FILING DATE: 1999-07-09
 33 <150> PRIOR APPLICATION NUMBER: USSN 09/400,492
 34 <151> PRIOR FILING DATE: 1999-09-21
 36 <150> PRIOR APPLICATION NUMBER: USSN 09/399,913
 37 <151> PRIOR FILING DATE: 1999-09-21
 39 <150> PRIOR APPLICATION NUMBER: PCT/US99/27428
 40 <151> PRIOR FILING DATE: 1999-11-19
 43 <160> NUMBER OF SEQ ID NOS: 73
 45 <170> SOFTWARE: PatentIn Ver. 2.0
 47 <210> SEQ ID NO: 1
 48 <211> LENGTH: 1463
 49 <212> TYPE: DNA
 50 <213> ORGANISM: Homo sapiens
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 53 <221> NAME/KEY: CDS
 54 <222> LOCATION: (225)..(872)
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 58 gaatagcccc ctttcacttc tgagtccctg catgtgcggg gctgaagaag gaagccagaa 60
                                                    Met Gly Ala Val
 66                                                   1
 68 atg ggc acc ttc tca tct ctg caa acc aaa caa agg cga ccc tcg aaa   284
 69 Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg Arg Pro Ser Lys
 70   5                  10                  15                  20
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See page 5

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Input Set : **A:\seqlistcorrected.txt**
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                      25                        30                        35
gag gga ctg gag cag ctc gag gcc cag acc aac ttc acc aag agg gag    380
Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg Glu
                40                        45                        50
ctg cag gtc ctt tat cga ggc ttc aaa aat gag tgc ccc agt ggt gtg    428
Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val
            55                        60                        65
gtc aac gaa gac aca ttc aag cag atc tat gct cag ttt ttc cct cat    476
Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His
        70                        75                        80
gga gat gcc agc acg tat gcc cat tac ctc ttc aat gcc ttc gac acc    524
Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr
 85                        90                        95                       100
act cag aca ggc tcc gtg aag ttc gag gac ttt gta acc gct ctg tcg    572
Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser
                    105                       110                       115
att tta ttg aga gga act gtc cac gag aaa cta agg tgg aca ttt aat    620
Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn
                120                       125                       130
ttg tat gac atc aac aag gac gga tac ata aac aaa gag gag atg atg    668
Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met
            135                       140                       145
gac att gtc aaa gcc atc tat gac atg atg ggg aaa tac aca tat cct    716
Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro
        150                       155                       160
gtg ctc aaa gag gac act cca agg cag cat gtg gac gtc ttc ttc cag    764
Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln
165                       170                       175                       180
aaa atg gac aaa aat aaa gat ggc atc gta act tta gat gaa ttt ctt    812
Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe Leu
                    185                       190                       195
gaa tca tgt cag gag gac gac aac atc atg agg tct ctc cag ctg ttt    860
Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu Phe
                200                       205                       210
caa aat gtc atg taactggtga cactcagcca ttcagctctc agagacattg        912
Gln Asn Val Met
            215
tactaaacaa ccaccttaac accctgatct gcccttgttc tgattttaca caccaactct 972
tgggacagaa acacctttta cactttggaa gaattctctg ctgaagactt tcttatggaa 1032
cccagcatca tgtggctcag tctctgattg ccaactcttc ctctttcttc ttcttgagag 1092
agacaagatg aaatttgagt ttgttttgga agcatgctca tctcctcaca ctgctgccct 1152
atggaaggtc cctctgctta agcttaaaca gtagtgcaca aaatatgctg cttacgtgcc 1212
[illegible]
[illegible]
cagcacctaa catatgtggg ataggactga attattaagc atgacattgt ctgatgaccc 1452
aaactgcccc g                                                      1463
<210> SEQ ID NO: 2
<211> LENGTH: 216
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RAW SEQUENCE LISTING DATE: 07/05/2001
PATENT APPLICATION: US/09/670,756A TIME: 10:39:36

Input Set : A:\seqlistcorrected.txt
Output Set: N:\CRF3\07052001\I670756A.raw

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147 <212> TYPE: PRT
148 <213> ORGANISM: Homo sapiens
150 <400> SEQUENCE: 2
151 Met Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg
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154 Arg Pro Ser Lys Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val
155              20                  25                  30
157 Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
158          35                  40                  45
160 Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
161      50                  55                  60
163 Pro Ser Gly Val Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln
164  65                  70                  75                  80
166 Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
167                  85                  90                  95
169 Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
170              100                 105                 110
172 Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg
173          115                 120                 125
175 Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
176      130                 135                 140
178 Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
179 145                 150                 155                 160
181 Tyr Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp
182                 165                 170                 175
184 Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu
185              180                 185                 190
187 Asp Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser
188          195                 200                 205
190 Leu Gln Leu Phe Gln Asn Val Met
191      210                 215
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195 <211> LENGTH: 1856
196 <212> TYPE: DNA
197 <213> ORGANISM: Rattus sp.
199 <220> FEATURE:
200 <221> NAME/KEY: CDS
201 <222> LOCATION: (300)..(1034)
203 <400> SEQUENCE: 3
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206 tcttggctag cagatgttta gggactggtt aagcctttgg agaaattacc ttaggaaaac 120
208 gggggaaataa aagcaaaaat taccatgaat tgcaagatta cctagcaatt gcaagggtagg 180
[illegible]
215 Met Pro Ala Arg Val Leu Leu Ala Tyr Pro Gly Thr Glu Met Leu Thr
216   1               5                  10                  15
218 cag ggc gag tct gaa ggg ctc cag acc ttg ggg ata gta gtg gtc ctg    395
219 Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu
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RAW SEQUENCE LISTING DATE: 07/05/2001
PATENT APPLICATION: US/09/670,756A TIME: 10:39:36

Input Set : A:\seqlistcorrected.txt
Output Set: N:\CRF3\07052001\I670756A.raw

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220                 20                  25                  30
222 tgt tcc tct ctg aaa cta ctg cac tac ctc ggg ctg att gac ttg tcg   443
223 Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser
224          35                  40                  45
226 gat gac aag atc gag gat gat ctg gag atg acc atg gtt tgc cat cgg   491
227 Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg
228      50                  55                  60
230 cct gag gga ctg gag cag ctt gag gca cag acg aac ttc acc aag aga   539
231 Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg
232  65                  70                  75                  80
234 gaa ctg caa gtc ctt tac cgg gga ttc aaa aac gag tgc ccc agt ggt   587
235 Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
236                  85                  90                  95
238 gtg gtt aac gaa gag aca ttc aag cag atc tac gct cag ttt ttc cct   635
239 Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro
240              100                 105                 110
242 cat gga gat gcc agc aca tac gca cat tac ctc ttc aat gcc ttc gac   683
243 His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp
244          115                 120                 125
246 acc acc cag aca ggc tct gta aag ttc gag gac ttt gtg act gct ctg   731
247 Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu
248      130                 135                 140
250 tcg att tta ctg aga gga acg gtc cat gaa aaa ctg agg tgg acg ttt   779
251 Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe
252 145                 150                 155                 160
254 aat ttg tac gac atc aat aaa gac ggc tac ata aac aaa gag gag atg   827
255 Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met
256                 165                 170                 175
258 atg gac ata gtg aaa gcc atc tat gac atg atg ggg aaa tac acc tat   875
259 Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr
260              180                 185                 190
262 cct gtg ctc aaa gag gac act ccc agg cag cac gtg gac gtc ttc ttc   923
263 Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe
264          195                 200                 205
266 cag aaa atg gat aaa aat aaa gat ggc att gta acg tta gac gaa ttt   971
267 Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe
268      210                 215                 220
270 ctc gag tcc tgt cag gag gat gac aac atc atg agg tct cta cag ctg  1019
271 Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu
272 225                 230                 235                 240
274 ttc caa aat gtc atg taactgagga cactggccat cctgctctca gagacactga  1074
275 Phe Gln Asn Val Met

282 cgagtggctc agtctctgat tgccaagctc tcctccctcc tcctcttgaa agggacgagc 1254
284 tgaaatccga agtttgtttt ggaagcatgc ccatctctcc atgctgctgc tgccctgtgg 1314
286 aaggccccta tgcttgagct taaacagtag tgcacagttt tctgcgtata cagatcccca 1374
288 actcactgcc tctaagtcag gcagaccctg atcaatctga accaaatgtg caccatcctc 1434
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RAW SEQUENCE LISTING DATE: 07/05/2001
PATENT APPLICATION: US/09/670,756A TIME: 10:39:36

Input Set : A:\seqlistcorrected.txt
Output Set: N:\CRF3\07052001\I670756A.raw

290 cgatggcctc ccaagccaat gtgcctgctt ctcttcctct ggtgggaaga aagaacgctc 1494
292 tacagagcac ttagagctta ccatgaaaat actgggagag gcagcaccta acacatgtag 1554
294 aataggactg aattattaag catggtggta tcagatgatg caaacagccc atgtcatttt 1614
296 tttttccaga ggtagggact aataattctc ccacactagc acctacgatc atagaacaag 1674
298 tctttttaaca catccaggag ggaaaccgct gcccagtggt ctatcccttc tctccatccc 1734
300 ctgctcaagc ccagcactgc atgtctctcc cggaaggtcc agaatgcctg tgaaatgctg 1794
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304 aa 1856
307 <210> SEQ ID NO: 4
308 <211> LENGTH: 245
309 <212> TYPE: PRT
310 <213> ORGANISM: Rattus sp.
312 <400> SEQUENCE: 4
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316 Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu
317 20 25 30
319 Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser
320 35 40 45
322 Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg
323 50 55 60
325 Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg
326 65 70 75 80
328 Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
329 85 90 95
331 Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro
332 100 105 110
334 His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp
335 115 120 125
337 Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu
338 130 135 140
340 Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe
341 145 150 155 160
343 Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met
344 165 170 175
346 Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr
347 180 185 190
349 Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe
350 195 200 205
352 Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe
353 210 215 220
[illegible] Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu
362 <210> SEQ ID NO: 5
363 <211> LENGTH: 1907
364 <212> TYPE: DNA
365 <213> ORGANISM: Mus musculus

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 07/05/2001
PATENT APPLICATION: **US/09/670,756A** TIME: 10:39:37

Input Set : **A:\seqlistcorrected.txt**
Output Set: **N:\CRF3\07052001\I670756A.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
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L:878 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:936 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:3017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:3353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:3356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43